

210. Plant-Microbe Interfaces: Constructed plant and bacterial communities for understanding and predicting community function.

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Project Goals: The goal of the PMI SFA is to understand the genome-dependent molecular and cellular events involved in establishing and maintaining beneficial interactions between plants and microbes. Populus and its associated microbial community serves as the experimental system for understanding how these molecular events manifest themselves within the spatially, structurally, and temporally complex scales of natural systems. To achieve this goal, we focus on 1) characterizing host and environmental drivers for diversity and function in the Populus microbiome, 2) utilizing microbial model system studies to elucidate Populus-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships and 3) develop metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the Populus-microbial interface.

Our goal is to study and understand the community function of the Populus host plant and its associated microbiome by leveraging our 1,039 genome sequenced Populus clones, collection of >2700 bacterial isolates, functional genomic and physiological assays from plants with individual microbes, and community data from wild Populus trees. Our results indicate that strains alone and in combinations of 10 or less can have a drastic influence on plant morphology and biochemistry. For example, the colonization of *Pseudomonas fluorescens* strain GM41 on plant roots has a strong effect on leaf metabolome profiles. This effect is also observed in combination with *Burkholderia* sp. BT03, which increases root biomass in individual and four member communities. The abundance of GM41 and BT03 are equal in individual or mixed experiments, suggesting that these strains occupy different root regions or niche space. As an initial attempt to model plant-microbe interactions, we recently coupled an N-fixing metabolic model of a diazotrophic endophyte with a plant host physiological model to inform nitrogen status and constrain the uncertainty surrounding net photosynthesis predictions and community biomass estimates. To extend this model and further evaluate how host carbon status influences the microbiome, we recently imposed a light stress limitation that altered carbon allocation patterns. We are currently investigating how this treatment will influence root exudate composition and concentration that are growth substrates for the microbiome. These data and modeling endeavors will be used to generate hypotheses for testing community biodesign strategies for sustainable bioenergy feedstock production.

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